

## Problem L

# Molecular scissors

*Source file:* molecularscissors.{ c | cpp | java | py }  
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Within the universe of molecular biology, there exist special molecules called enzymes that act as catalysts for biochemical reactions. A specific family of enzymes, known as restriction enzymes, have a unique affinity for specific sequences of nucleotides in a strand of DNA. These enzymes "read" the DNA strand and cut it at their respective recognition sites, acting as molecular scissors.

Scientists have discovered a unique characteristic of the recognition sites of certain enzymes, particularly restriction enzymes. The nucleotide sequence on one strand, when read from a specific direction, matches the sequence on the complementary strand, read in the opposite direction.

For example:

Strand: AAGCTT

Complementary: TTCGAA

As shown, reading the strand from left to right is identical to reading the complementary strand from right to left.

Conversely, a strand like the following does not exhibit this characteristic:

Strand: AAGG

Complementary: TTCC

Restriction enzymes can cut sequences like AAGCTT and its complementary TTCGAA, but not sequences like AAGG and TTCC. As real examples, the restriction enzyme EcoRI recognizes the sequence GAATTC, and its complementary strand would read CTTAAG. Similarly, the enzyme HindIII recognizes the sequence AAGCTT and the complementary strand reading TTCGAA. These enzymes are crucial in molecular biology, allowing scientists to cut DNA strands at specific locations, facilitating various genetic engineering and research applications.

As a Bioinformatics intern, your task is to develop a program to assist researchers in identifying potential recognition sites (inside of a strand) for such a type of enzymes. The program should identify sequences that exhibit the aforementioned characteristic.

### Input:

The input consists of multiple lines, each representing a DNA sequence, composed of the characters A, T, C, and G, representing the nucleotides Adenine, Thymine, Cytosine, and Guanine respectively. The maximum length of each DNA sequence is  $10^5$ . The input ends with EOF.

### Output:

For each DNA sequence, if no site (part of the sequence) that can be matched by a restriction enzyme is found, output "false". If such a site is found, output the starting position and the length of the longest such sequence within the DNA strand. If more than one site presents the same length, present the starting position and the length of the first one.

**Example:**

**Input:**

Example of Input 1	Example of Output 1
GAATTC	1 6
AAGCTTTCGAAGCTTAAAAAA	1 6
CCGGAAGGCCGG	1 4
ATT	false
AAGCTCAA	2 4
AA	false
AAGG	false